

AMENDMENTS TO THE CLAIMS

This listing of the claims replaces all prior listings and versions:

1 to 272. (canceled).

273. (currently amended) A population of host cells, each host cell comprising:

(a) a polynucleotide encoding a fusion protein, the fusion protein comprising

(i) an activation tag; and

(ii) a polypeptide sequence to be assayed for its interaction with a DNA sequence,

(b) a transcriptional regulatory sequence comprising one or more binding sites for a zinc finger DNA-binding domain;

(c) a reporter gene operably linked to the transcriptional regulatory sequence, wherein expression of the reporter gene is modulated when the polypeptide sequence interacts with one or more of the binding sites;

wherein at least 10^7 unique pairs of a the one or more binding sites and a fusion proteins that bind to the 10^7 unique pairs of the one or more binding sites are represented in the population of host cells.

274. (previously presented) The population of host cells according to claim 273, wherein the cells are prokaryotic cells.

275. (currently amended) The population of host cells according to claim 273, wherein expression of the reporter gene confers a growth advantage on a host cell of the population in which host cell the polypeptide sequence interacts with the one or more binding sites.

276. (previously presented) The population of host cells according to claim 273, wherein the activation tag comprises an RNA polymerase, an RNA polymerase subunit, a functional fragment of an RNA polymerase, or a functional fragment of an RNA polymerase subunit.

277. (previously presented) The population of host cells according to claim 273, wherein the activation tag covalently or non-covalently interacts with an RNA polymerase, an RNA polymerase subunit, a functional fragment of RNA polymerase, or a functional fragment of an RNA polymerase subunit.

278. (previously presented) The population of host cells according to claim 273, wherein the activation tag interacts indirectly with RNA polymerase via at least one intermediary polypeptide, nucleic acid, or small molecule, which functionally links the activation tag to the RNA polymerase.

279. (previously presented) The population of host cells according to claim 273, wherein an intermediary peptide is covalently fused to an RNA polymerase, an RNA polymerase subunit, a functional fragment of RNA polymerase, or a functional fragment of an RNA polymerase subunit.

280. (previously presented) The population of host cells according to claim 277, wherein the activation tag comprises a fragment of Gal11P which non-covalently interacts with a fusion polypeptide comprising an RNA polymerase, an RNA polymerase subunit, a functional fragment of RNA polymerase, or a functional fragment of an RNA polymerase subunit.

281. (previously presented) The population of host cells according to claim 280, wherein the fusion polypeptide further comprises Gal4.

282. (previously presented) The population of host cells according to claim 273, wherein (a), (b), or (a) and (b), are contained within one or more vectors in the host cell.

283. (previously presented) The population of host cells according to claim 275, wherein the growth advantage is relief of a cell nutritional requirement.

284. (previously presented) The population of host cells according to claim 275, wherein the degree of the growth advantage conferred by the desired level of expression of the reporter gene is controllable by varying the growth conditions of the host cell.

285. (previously presented) The population of host cells according to claim 283, wherein the reporter gene is the yeast His3 gene.

286. (previously presented) The population of host cells according to claim 285, wherein the degree of the growth advantage is controllable by exposing the host cell to varying concentrations of 3-aminotriazole.

287. (original) The population of host cells according to claim 275, wherein the reporter gene is a β -lactamase gene.

288. (original) The population of host cells according to claim 287, wherein the β -lactamase gene is TEM-1.

289. (original) The population of host cells according to claim 287, wherein the degree of the growth advantage is controllable by exposing the host cell to a β -lactam antibiotic.

290. (original) The population of host cells according to claim 284, wherein the reporter gene is a β -lactamase gene and the degree of the growth advantage is controllable by exposing the host cell to a β -lactam antibiotic and varying concentrations of a β -lactamase inhibitor.

291. (original) The population of host cells according to claim 290, wherein the β -lactam antibiotic is a penicillin.

292. (original) The population of host cells according to claim 290, wherein the β -lactamase inhibitor is Clavulanic acid.

293. (currently amended) The population of host cells according to claim 273, wherein the binding site is a member of a library of at least 10^7 potential binding sites for a zinc finger DNA binding domain.

294. (currently amended) The population of host cells according to claim 273, wherein the binding site is a member of a library of at least 10^8 potential binding sites for a zinc finger DNA binding domain.

295. (canceled)

296. (previously presented) The population of host cells according to claim 273, wherein the polypeptide sequence to be assayed is a member of a library of at least 10^7 polypeptides.

297. (currently amended) The population of host cells according to claim 296, wherein the polypeptide sequence to be assayed is a member of a library of at least 10^8 polypeptides.

298. (canceled)

299. (currently amended) A method for detecting an interaction between a polypeptide sequence and a DNA sequence, comprising

providing a population of host cells according to claim 273;
assaying the population of host cells for expression of the reporter gene;
identifying host cells in which expression of the reporter gene is modulated, thereby detecting interaction between the polypeptide sequence and the zinc finger DNA-binding domain DBD recognition element in the host cell.

300. (original) The method of claim 299, further comprising the step of identifying the polynucleotide encoding the fusion protein.